CLAIMS

1. A method of constructing a variant of a parent *Coprinus* laccase, which variant has laccase activity and increased oxidation potential and/or altered pH optimum and/or altered mediator pathway and/or altered O_2/OH^--pathway as compared to said parent laccase, which method comprises

i) analysing the three-dimensional structure of the parent *Coprinus* laccase to identify at least one amino acid residue or at least one structural part of the *Coprinus* laccase structure, which amino acid residue or structural part is believed to be of relevance for altering the oxidation potential and/or altering the pH optimum and/or altering the mediator pathway and/or altering the O_2/OH^--pathway of the parent *Coprinus* laccase (as evaluated on the basis of structural or functional considerations),

ii) constructing a *Coprinus* laccase variant, which as compared to the parent *Coprinus* laccase, has been modified in the amino acid residue or structural part identified in i) so as to alter the oxidation potential and/or alter the pH optimum and/or alter the mediator pathway and/or alter the O_2/OH^--pathway, and, optionally,

iii) testing the resulting *Coprinus* laccase variant with respect to oxidation potential and/or pH optimum and/or mediator pathway and/or O_2/OH^--pathway.

2. A variant of a parent *Coprinus* laccase, which variant has increased oxidation potential and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 1:
G411A,V,P,L,I,F,Y,W;
G412A,V,P,L,I,F,Y,W;
V409P,L,I,F,Y,W;
T257A,V,P,L,I,F,Y,W;

F358Y,W,I;
T359A,V,P,L,I,F,Y,W;
L480I,F,Y,W;
L351 I,F,Y,W;
E473A,V,P,L,I,F,Y,W;
D98A,V,P,L,I,F,Y,W;
G131A,V,P,L,I,F,Y,W;
D443A,V,P,L,I,F,Y,W;
R260 A,V,P,L,I,F,Y,W.

3. A variant of a parent *Coprinus* laccase, which variant has an altered pH optimum and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 1:
180-181;
222-224;
257;
281-284;
352-353;
357-358;
409-416;
470-490.

4. A variant of a parent *Coprinus* laccase, which variant has an altered mediator efficiency and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 1:
179-182;
223;
281-282;
353-358;
410-412;
472;
474-475;
477-478.

5. A method of constructing a variant of a parent *Coprinus*-like laccase, which variant has laccase activity and increased

oxidation potential and/or changed pH optimum and/or altered mediator pathway and/or altered O_2/OH^--pathway as compared to said parent laccase, which method comprises

i) comparing the three-dimensional amino acid structure of the *Coprinus* laccase with an amino acid sequence of a *Coprinus*-like laccase,

ii) identifying a part of the *Coprinus*-like laccase amino acid sequence which is different from the *Coprinus* laccase amino acid sequence and which from structural or functional considerations is contemplated to be responsible for differences in the stability of the *Coprinus* and *Coprinus*-like laccase,

iii) modifying the part of the *Coprinus*-like laccase identified in ii) whereby a *Coprinus*-like laccase variant is obtained, which has an increased oxidation potential and/or changed pH optimum and/or altered mediator pathway and/or altered O_2/OH^--pathway as compared to the parent *Coprinus*-like laccase, and optionally,

iv) testing the resulting *Coprinus*-like laccase variant with respect to oxidation potential and/or pH optimum and/or mediator pathway and/or O_2/OH^-pathway.

6. The method according to claim 5, wherein, in step iii), the part of the *Coprinus*-like laccase is modified so as to resemble the corresponding part of the *Coprinus* laccase.

7. The method according to claim 5 or 6, wherein, in step iii), the modification is accomplished by deleting one or more amino acid residues of the part of the *Coprinus*-like laccase to be modified; or the modification is accomplished by replacing one or more amino acid residues of the part of the *Coprinus*-like laccase to be modified with the amino acid residues occupying corresponding positions in the *Coprinus* laccase; or the

modification is accomplished by insertion of one or more amino acid residues present in the *Coprinus* laccase into a corresponding position in the *Coprinus*-like laccase.

8. The method according to any of claims 5-7, wherein the *Coprinus*-like laccase is selected from the group consisting of *Polyporus pinsitus* laccase, *Phlebia radiata* laccase, *Rhizoctonia solani* laccase, *Scytalidium thermophilum* laccase and *Myceliophthora thermophila* laccase.

9. The method according to claim 1 or 5, wherein the parent *Coprinus* laccase is derived from a strain of *Coprinus cinereus*.

10. The method according to claim 9, wherein the parent *Coprinus* laccase is derived from *Coprinus cinereus* IFO 8371.

11. A variant of a parent *Polyporus pinsitus (I)* laccase, which variant has an increased oxidation potential and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 2:
A390V,P,L,I,F,Y,W;
G392A,V,P,L,I,F,Y,W;
E460D.

12. A variant of a parent *Polyporus pinsitus (I)* laccase, which variant has an altered pH optimum and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 2:
E460L,I,F,M,S;
F463L,M.

13. A variant of a parent *Polyporus pinsitus (I)* laccase, which variant has an altered mediator efficiency and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 2:
G392A;

A461T,S;
N260Q,Y;
G165K,R.

14. A variant of a parent *Polyporus pinsitus (I)* laccase, which variant has an altered O_2/OH^-pathway and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 2:
F81D,E;
L112D,E;
A80D,E.

15. A variant of a parent *Myceliophthora thermophila* laccase, which variant has an increased oxidation potential and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 10:
G511A,V,P,L,I,F,Y,W;
T428A,V,P,L,I,F,Y,W;
S510A,V,P,L,I,F,Y,W;
D106A,V,P,L,I,F,Y,W;
N109A,V,P,L,I,F,Y,W,Q;
L500I,F,Y,W;
A108V,P,L,I,F,Y,W;
G514A,V,P,L,I,F,Y,W.

16. A variant of a parent *Myceliophthora thermophila* laccase, which variant has an altered pH optimum and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 10:
192-193;
234-236;
269;
293-294;
364-365;
372-373;
426-433;
503-513.

17. A variant of a parent *Myceliophthora thermophila* laccase, which variant has an altered mediator efficiency and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 10:
185-194;
235;
293-294;
365-373;
427-429;
505;
507-508;
510-511.

18. A variant of a parent *Myceliophthora thermophila* laccase, which variant has an altered O_2/OH^--pathway and comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 10:
A506E;
N109D;
H93E;
H95E;
M433E;
M480E.

19. A DNA construct comprising a DNA sequence encoding a laccase variant according to claim 2 or claims 11-18.

20. A recombinant expression vector which carries a DNA construct according to claim 19.

21. A cell which is transformed with a DNA construct according to claim 19 or a vector according to claim 20.

22. A cell according to claim 21, which is a microorganism.

23. A cell according to claim 22, which is a bacterium or a fungus.

24. A cell according to claim 23, which is an *Aspergillus niger* or an *Aspergillus oryzae* cell.

25. Use of a laccase variant according to claim 2 or claims 11-18 for oxidizing a substrate.

26. Use of a laccase variant according to claim 2 or claims 11-18 for dye transfer inhibition.

27. Use of a laccase variant according to claim 2 or claims 11-18 for bleaching textiles, in particular for bleaching denim.

28. A detergent additive comprising a laccase variant according to claim 2 or claims 11-18 in the form of a non-dusting granulate, a stabilised liquid or a protected enzyme.

29. A detergent additive according to claim 28, which additionally comprises one or more other enzyme such as a protease, a lipase, an amylase, and/or a cellulase.

30. A detergent composition comprising a laccase variant according to claim 2 or claims 11-18 and a surfactant.

31. A detergent composition according to claim 30 which additionally comprises one or more other enzymes such as a protease, a lipase, an amylase and/or a cellulase.